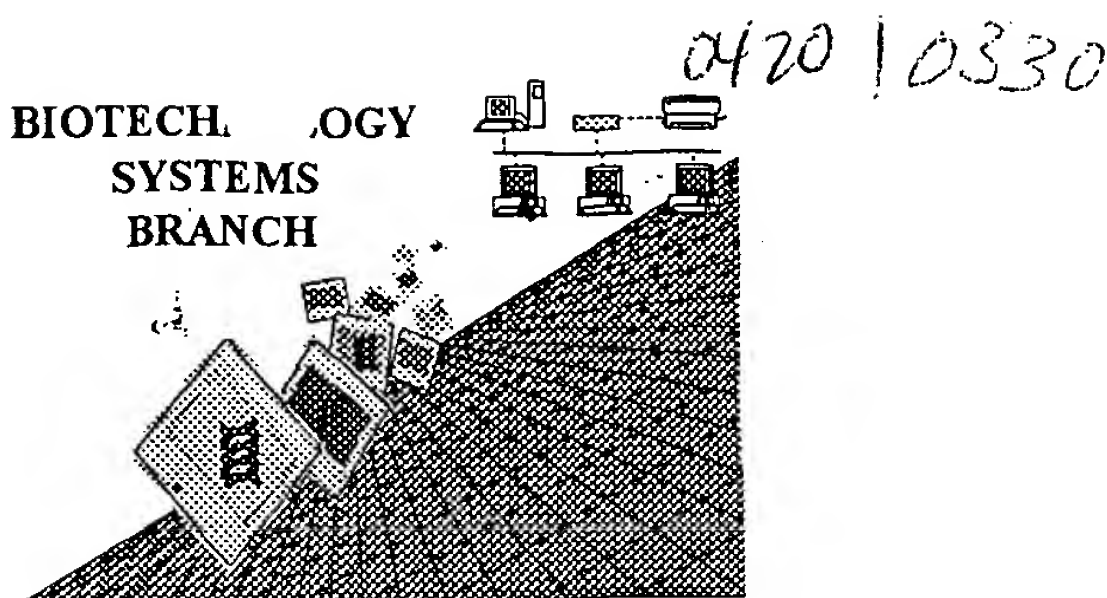


## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECH. .OGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/883,848

Source: O/PE

Date Processed by STIC: 10/12/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/883,848

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length  
Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)  
Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)  
Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9      Use of n's or Xaa's  
    (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>  
Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/883,848

DATE: 10/12/2001

TIME: 12:14:38

Input Set : A:\CIBT-P01-119 Seq List.txt

Output Set: N:\CRF3\10122001\I883848.raw

Does Not Comply  
Corrected Diskette Needed

pg 1,3

3 <110> APPLICANT: Ling, L.  
 4 Sanicola-Nadel, M.  
 6 <120> TITLE OF INVENTION: ANGIOGENESIS-MODULATING COMPOSITIONS AND USES  
 8 <130> FILE REFERENCE: CIBT-P01-119  
 10 <140> CURRENT APPLICATION NUMBER: 09/883,848  
 11 <141> CURRENT FILING DATE: 2001-09-24  
 13 <150> PRIOR APPLICATION NUMBER: 60/211,919  
 14 <151> PRIOR FILING DATE: 2000-06-16  
 16 <160> NUMBER OF SEQ ID NOS: 48  
 18 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORED SEQUENCES

167 <210> SEQ ID NO: 6  
 168 <211> LENGTH: 1425  
 169 <212> TYPE: DNA  
 170 <213> ORGANISM: Homo sapiens  
 172 <400> SEQUENCE: 6  
 173 atgctgctgc tggcgagatg tctgctgcta gtccctcgtct cctcgtctgct ggtatgctcg 60  
 174 ggactggcgt gcggaccggg caggggggttc gggaagagga ggcaccccaa aaagctgacc 120  
 175 ccttttagcct acaagcagtt tatccccaat gtggccgaga agaccctagg cgccagcgga 180  
 176 aggtatgaag ggaagatctc cagaaactcc gagcgattta aggaactcac cccaattac 240  
 177 aaccccgaca tcatatttaa ggatgaagaa aacaccggag cggacaggct gatgactcag 300  
 178 aggtgtaagg acaagttgaa cgctttggcc atctcgggtga tgaaccagt ggcaggagt 360  
 179 aaactgcggg tgaccgaggg ctgggacgaa gatggccacc actcagagga gtctctgcac 420  
 180 tacgagggcc gcgcagtgga catcaccacg tctgaccgcg accgcagcaa gtacggcatg 480  
 181 ctggcccgcg tggcggtgga ggccggcttc gactgggtgt actacgagtc caaggcacat 540  
 182 atccactgct cgggtgaaagc agagaactcg gtggcggccca aatcgggagg ctgcttccc 600  
 183 ggctcggcca cgggtgcacct ggagcagggc ggcaccaagc tgggtgaagga cctgagcccc 660  
 184 ggggaccgcg tgctggcggc ggacgaccag ggccggctgc tctacagcga cttcctcact 720  
 185 ttcttgacc gcgacgacgg cgccaagaag gtcttctacg tgatcgagac gcgggagccg 780  
 186 cgcgagcgcc tgctgctcac cgccgcgcac ctgctctttg tggcgccgca caacgactcg 840  
 187 gccaccgggg agcccagagg gtccctcggg tcggggccgc cttccggggg cgcactgggg 900  
 188 cctcggggcg tgttcgccag ccgcgtgcgc ccggggccag gcgtgtacgt ggtggccgag 960  
 189 cgtgacgggg accgccggct cctgcccgcg gctgtgcaca gcgtgacct aagcgaggag 1020  
 190 gccgcggggc cctacgcgcc gctcacggcc cagggcacca ttctcatcaa ccgggtgctg 1080  
 191 gcctcgtgct acgcggtcat cgaggagcac agctgggcgc accgggcctt cgcgcccttc 1140  
 192 cgcctggcgc acgcgtcct ggctgactg gcgccgcgc gcacggaccg cggcggggac 1200  
 193 agcggcggcg gggaccgcgg gggcggcggc ggcagagtag ccctaaccgc tccagggtgct 1260  
 194 gccgacgctc cgggtgcggg ggccaccgcg ggcattccact ggtactcgca gctgctctac 1320  
 195 caaataggca cctggctcct ggacagcgag gccctgcacc cgctgggcat ggcggtcaag 1380  
 E--> 196 tccagcnnna gccggggggc cgggggaggg gcgcgggagg gggcc 1425

728 <210> SEQ ID NO: 15  
 729 <211> LENGTH: 475  
 730 <212> TYPE: PRT  
 731 <213> ORGANISM: Homo sapiens

P.3

→ see  
 item 9  
 on Error  
 Summary Sheet

## RAW SEQUENCE LISTING

DATE: 10/12/2001

PATENT APPLICATION: US/09/883,848

TIME: 12:14:38

Input Set : A:\CIBT-P01-119 Seq List.txt

Output Set: N:\CRF3\10122001\I883848.raw

```

733 <400> SEQUENCE: 15
734 Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu
735   1           5           10           15
737 Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys
738           20           25           30
740 Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
741           35           40           45
743 Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
744           50           55           60
746 Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
747   65           70           75           80
749 Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
750           85           90           95
752 Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser
753           100          105          110
755 Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
756           115          120          125
758 Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg
759           130          135          140
761 Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met
762 145           150          155          160
764 Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
765           165          170          175
767 Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
768           180          185          190
770 Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu
771           195          200          205
773 Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly Asp Arg Val
774           210          215          220
776 Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu Thr
777 225           230          235          240
779 Phe Leu Asp Arg Asp Asp Gly Ala Lys Lys Val Phe Tyr Val Ile Glu
780           245          250          255
782 Thr Arg Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu Leu
783           260          265          270
785 Phe Val Ala Pro His Asn Asp Ser Ala Thr Gly Glu Pro Glu Ala Ser
786           275          280          285
788 Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu
789           290          295          300
791 Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu
792 305           310          315          320
794 Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr
795           325          330          335
797 Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly
798           340          345          350
800 Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu
801           355          360          365
803 Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His
804           370          375          380

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/883,848

DATE: 10/12/2001

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Input Set : A:\CIBT-P01-119 Seq List.txt

Output Set: N:\CRF3\10122001\I883848.raw

806 Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp  
 807 385 390 395 400  
 809 Ser Gly Gly Gly Asp Arg Gly Gly Gly Gly Gly Arg Val Ala Leu Thr  
 810 405 410 415  
 812 Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile  
 813 420 425 430  
 815 His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp  
 816 435 440 445  
 E--> 818 Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser  
 819 450 455 460  
 821 Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala  
 822 465 470 475  
 1348 <210> SEQ ID NO: 23  
 1349 <211> LENGTH: 174 175 shown  
 1350 <212> TYPE: PRI  
 1351 <213> ORGANISM: Homo sapiens  
 1353 <400> SEQUENCE: 23  
 1354 Cys Gly Pro Gly Arg Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys  
 1355 1 5 10 15  
 1357 Leu Val Pro Leu Ala Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys  
 1358 20 25 30  
 1360 Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser  
 1361 35 40 45  
 1363 Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe  
 1364 50 55 60  
 1366 Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys  
 1367 65 70 75 80  
 1369 Lys Asp Arg Leu Asn Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro  
 1370 85 90 95  
 1372 Gly Val Lys Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His His  
 1373 100 105 110  
 1375 Ser Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr  
 1376 115 120 125  
 1378 Ser Asp Arg Asp Arg Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val  
 1379 130 135 140  
 1381 Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Lys Ala His Val His  
 1382 145 150 155 160  
 1384 Cys Ser Val Lys Ser Glu His Ser Ala Ala Lys Thr Gly Gly  
 E--> 1385 165 170 175 ←

Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/883,848

DATE: 10/12/2001

TIME: 12:14:39

Input Set : A:\CIBT-P01-119 Seq List.txt

Output Set: N:\CRF3\10122001\I883848.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:196 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6  
L:818 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15  
L:1385 M:252 E: No. of Seq. differs, <211>LENGTH:Input:174 Found:175 SEQ:23  
L:1698 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1704 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1707 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1711 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1714 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26